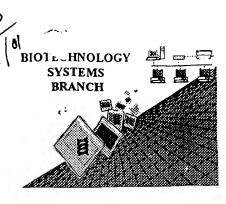# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/732,436

Source: OIPE

Date Processed by STIC: 4/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _// are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

RAW SEQUENCE LISTING   DATE: 04/16/2001
PATENT APPLICATION: US/09/732,436   TIME: 11:45:51

Input Set : A:\Cura-615.app
Output Set: N:\CRF3\04162001\I732436.raw

*Does Not Comply
Corrected Diskette Needed*

```
 3 <110> APPLICANT: Prayaga, Sudhirdas
 4         Shimkets, Richard
 6 <120> TITLE OF INVENTION: NOVEL INTERFERON OMEGA AND NUCLEIC ACIDS ENCODING SAME
 8 <130> FILE REFERENCE: 15966-615
10 <140> CURRENT APPLICATION NUMBER: 09/732,436
11 <141> CURRENT FILING DATE: 2000-12-07
13 <150> PRIOR APPLICATION NUMBER: 60/169,887
14 <151> PRIOR FILING DATE: 1999-12-09
16 <150> PRIOR APPLICATION NUMBER: 60/170,230
17 <151> PRIOR FILING DATE: 1999-12-10
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 475
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone
30         AC015663_A
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34  1               5                  10                  15
36 Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
37              20                  25                  30
39 Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
40          35                  40                  45
42 Cys Thr Ala Thr Thr Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys
43      50                  55                  60
45 Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys
46  65                  70                  75                  80
48 Ala Gly Gly Thr Gly Ala Thr Thr Thr Cys Thr Gly Cys Cys Cys Thr
49              85                  90                  95
51 Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly
52             100                 105                 110
54 Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr
55         115                 120                 125
57 Thr Thr Thr Thr Ala Cys Ala Cys Ala Ala Gly Gly Gly Cys Thr Thr
58      130                 135                 140
60 Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr
61 145                 150                 155                 160
63 Ala Gly Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala
64             165                 170                 175
66 Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr
67             180                 185                 190
69 Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala
70          195                 200                 205
72 Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr
```

```
73     210                   215                   220
75 Thr Thr Gly Gly Thr Ala Thr Ala Gly Ala Gly Gly Ala Thr Gly Gly
76 225             230                   235                   240
78 Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys
79             245                   250                   255
81 Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Gly Cys Cys
82             260                   265                   270
84 Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala
85         275                   280                   285
87 Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Gly Ala
88     290                   295                   300
90 Gly Thr Ala Cys Ala Thr Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala
91 305             310                   315                   320
93 Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala Ala Thr Thr Cys Ala Gly
94             325                   330                   335
96 Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Gly Ala Gly
97             340                   345                   350
99 Gly Thr Thr Gly Thr Cys Gly Thr Ala Ala Thr Gly Gly Thr Ala Ala
100         355                   360                   365
102 Ala Gly Gly Gly Ala Thr Thr Thr Thr Thr Cys Thr Thr Ala Ala Gly
103     370                   375                   380
105 Cys Ala Cys Ala Ala Ala Ala Cys Thr Thr Cys Ala Ala Gly Ala Ala
106 385             390                   395                   400
108 Ala Ala Ala Gly Ala Gly Ala Ala Cys Ala Gly Ala Ala Gly Ala Ala
109             405                   410                   415
111 Ala Ala Gly Ala Gly Ala Ala Cys Thr Gly Cys Ala Ala Ala Ala Ala
112             420                   425                   430
114 Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly Thr Ala
115         435                   440                   445
117 Ala Thr Cys Thr Ala Thr Thr Thr Ala Gly Cys Ala Gly Ala Ala Gly
118     450                   455                   460
120 Ala Gly Thr Gly Ala Ala Ala Gly Cys Thr Gly
121 465             470                   475
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 610
126 <212> TYPE: PRT
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone
132 <400> SEQUENCE: 2
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134  1               5                   10                  15
136 Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
137             20                  25                  30
139 Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
140         35                  40                  45
142 Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys
143     50                  55                  60
145 Gly Ala Cys Cys Thr Gly Cys Cys Thr Asn Asn Asn Asn Asn Asn Asn
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RAW SEQUENCE LISTING   DATE: 04/16/2001
PATENT APPLICATION: US/09/732,436   TIME: 11:45:51

Input Set : A:\Cura-615.app
Output Set: N:\CRF3\04162001\I732436.raw

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146  65                     70                  75                      80
148 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
149                 85                  90                  95
151 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
152             100                 105                 110
154 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
155         115                 120                 125
157 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
158     130                 135                 140
160 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
161 145                 150                 155                 160
163 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
164             165                 170                 175
166 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
167         180                 185                 190
169 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
170     195                 200                 205
172 Ala Ala Ala Gly Cys Thr Cys Ala Gly Gly Thr Gly Ala Thr Thr Thr
173     210                 215                 220
175 Cys Thr Gly Cys Cys Cys Thr Cys Cys Ala Thr Ala Ala Gly Ala Thr
176 225                 230                 235                 240
178 Gly Cys Ala Cys Cys Ala Gly Cys Ala Gly Ala Thr Cys Thr Thr Cys
179             245                 250                 255
181 Ala Gly Cys Cys Thr Cys Thr Thr Thr Thr Thr Ala Cys Ala Cys Ala
182         260                 265                 270
184 Ala Gly Gly Gly Cys Thr Thr Gly Thr Cys Thr Gly Ala Thr Gly Cys
185     275                 280                 285
187 Thr Thr Gly Gly Ala Ala Thr Ala Gly Gly Gly Cys Cys Thr Thr Cys
188     290                 295                 300
190 Cys Thr Gly Gly Ala Cys Ala Ala Ala Cys Thr Cys Cys Ala Gly Ala
191 305                 310                 315                 320
193 Cys Thr Gly Gly Ala Thr Thr Thr Cys Ala Thr Cys Ala Gly Cys Ala
194             325                 330                 335
196 Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys Thr Gly Gly Ala Gly
197         340                 345                 350
199 Ala Cys Cys Thr Gly Cys Thr Thr Thr Gly Gly Thr Ala Thr Ala Gly
200         355                 360                 365
202 Ala Gly Gly Ala Thr Gly Gly Gly Ala Ala Gly Cys Ala Ala Gly Ala
203     370                 375                 380
205 Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly Ala Ala Ala Thr Thr
206 385                 390                 395                 400
208 Gly Ala Gly Gly Gly Cys Cys Cys Thr Ala Cys Ala Cys Thr Gly Gly
209             405                 410                 415
211 Cys Cys Ala Thr Ala Ala Ala Gly Ala Gly Gly Thr Ala Cys Thr Thr
212         420                 425                 430
214 Cys Cys Ala Gly Gly Gly Ala Gly Thr Ala Cys Ala Thr Thr Thr Cys
215         435                 440                 445
217 Thr Thr Cys Thr Thr Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Ala
218     450                 455                 460
```

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220 Ala Ala Thr Thr Cys Ala Gly Gly Ala Ala Cys Thr Gly Thr Ala Cys
221 465                 470                 475                 480
223 Cys Thr Gly Gly Gly Ala Gly Gly Thr Thr Gly Thr Cys Gly Thr Ala
224                 485                 490                 495
226 Ala Thr Gly Gly Thr Ala Ala Ala Gly Gly Gly Ala Thr Thr Thr Thr
227                 500                 505                 510
229 Thr Cys Thr Thr Ala Ala Gly Cys Ala Cys Ala Ala Ala Ala Cys Thr
230         515                 520                 525
232 Thr Cys Ala Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys
233     530                 535                 540
235 Ala Gly Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys Thr
236 545                 550                 555                 560
238 Gly Cys Ala Ala Ala Ala Ala Ala Ala Ala Thr Cys Thr Gly Gly Ala
239                 565                 570                 575
241 Ala Ala Ala Gly Gly Thr Ala Ala Thr Cys Thr Ala Thr Thr Thr Ala
242                 580                 585                 590
244 Gly Cys Ala Gly Ala Ala Gly Ala Gly Thr Gly Ala Ala Ala Gly Cys
245         595                 600                 605
247 Thr Gly
248     610
251 <210> SEQ ID NO: 3
252 <211> LENGTH: 1887
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence: Curagen clone
258         AF038458_A
260 <400> SEQUENCE: 3
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262 cagtcagcca cacccagccc atgtccccgc cgctgccgct gccagacaca gtcgctgccc 120
263 ctaagcgtgc tgtgcccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgccgg 180
264 gcagccgagc tgcggctggc agacaacttc atcgcctccg tgcgccgccg cgacctggcc 240
265 aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
266 ggcgccttcg ccgacctgcg ggccctgcgt gccctgcacc tggatggcaa ccggctgacc 360
267 tcactgggcg agggccagct cgcggcctg  gtcaacttgc gccacctcat cctcagcaac 420
268 aaccagctgg cagcgctggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
269 ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggccctggg ccgcctgggc 540
270 aacgtcaaca cgttgggcct cgaccacaac ctgctggctt ctgtgcccgc cggcgctttt 600
271 tcccgcctgc acaagctggc ccggctggac atgacctcca accgcctgac cacaatccca 660
272 cccgacccac tcttctcccg cctgcccctg ctcgccaggc cccggggctc gcccgcctct 720
273 gccctggtgc tggcctttgg cgggaacccc ctgcactgca actgcgagct ggtgtggctg 780
274 cgtcgcctgg cgcgggagga cgacctcgag gcctgcgcgt ccccacctgc tctgggcggc 840
275 cgctacttct gggcggtggg cgaggaggag tttgtctgcg agccgcccgt ggtgactcac 900
276 cgctcaccac ctctggctgt gcccgcaggt cggccggctg ccctgcgctg ccgggcagtg 960
277 ggggacccag agccccgtgt gcgttgggtg tcaccccagg gccggctgct aggcaactca 1020
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282 gccgacactg ggcccccctac cgaccgtggc gtccaggtga ctgagcacgg ggccacagct 1320
283 gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgta ccagatccag 1380
284 tacaacagct cggctgatga catcctcgtc tacaggatga tcccggcgga gagccgctcg 1440
285 ttcctgctga cggacctggc gtcaggccgg acctacgatc tgtgcgtgct cgccgtgtat 1500
286 gaggacagcg ccacggggct cacggccacg cggcctgtgg gctgcgcccg cttctccacc 1560
287 gaacctgcgc tgcggccatg cggggcgccg cacgctccct tcctgggcgg cacgatgatc 1620
288 atcgcgctgg gcggcgtcat cgtagcctcg gtactggtct tcatcttcgt gctgctaatg 1680
289 cgctacaagg tgcacggcgg ccagcccccc ggcaaggcca agattcccgc gcctgttagc 1740
290 agcgtttgct cccagaccaa cggcgccctg ggccccacgc ccacgcccgc cccgcccgcc 1800
291 ccggagcccg cggcgctcag ggcccacacc gtggtccagc tggactgcga gccctggggg 1860
292 cccggccacg aacctgtggg accctag                                    1887
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 365
296 <212> TYPE: PRT
297 <213> ORGANISM: Equus caballus
299 <400> SEQUENCE: 4
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301   1               5                   10                  15
303 Cys Gly Cys Gly Thr Cys Thr Gly Thr Cys Cys Thr Cys Cys Ala Cys
304               20                  25                  30
306 Gly Ala Gly Ala Thr Gly Cys Thr Cys Cys Ala Gly Cys Ala Gly Ala
307           35                  40                  45
309 Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr Thr Cys Cys Ala
310       50                  55                  60
312 Cys Ala Cys Ala Gly Ala Gly Cys Gly Cys Thr Cys Gly Thr Cys Thr
313   65                  70                  75                  80
315 Gly Cys Thr Gly Cys Cys Thr Gly Gly Ala Ala Cys Ala Cys Gly Ala
316               85                  90                  95
318 Cys Cys Cys Thr Cys Cys Thr Gly Gly Ala Cys Gly Ala Ala Cys Thr
319               100                 105                 110
321 Cys Thr Gly Cys Ala Cys Gly Gly Gly Ala Cys Thr Cys Cys Thr Thr
322           115                 120                 125
324 Cys Gly Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys
325       130                 135                 140
327 Thr Gly Gly Ala Cys Ala Cys Cys Thr Gly Thr Thr Thr Gly Gly Ala
328 145                 150                 155                 160
330 Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Gly Gly Ala Gly Ala Gly
331               165                 170                 175
333 Gly Ala Ala Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly
334           180                 185                 190
336 Gly Ala Ala Cys Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Ala Cys
337           195                 200                 205
339 Ala Cys Thr Gly Gly Cys Cys Gly Thr Gly Ala Ala Gly Ala Gly Gly
340       210                 215                 220
342 Thr Ala Cys Thr Thr Cys Cys Gly Gly Gly Gly Gly Ala Thr Cys Cys
343 225                 230                 235                 240
345 Ala Thr Cys Thr Cys Thr Ala Cys Cys Thr Gly Ala Ala Ala Gly Ala
346               245                 250                 255
348 Gly Ala Ala Gly Ala Ala Ala Thr Ala Cys Ala Gly Thr Gly Ala Cys
```

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<210> 8

<211> 70

<212> DNA

<213> Unknown


<220>

<223> Description of Unknown Organism: Interferon Alpha

      Precursor


<400> 8
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see item 10 on Err Summary Sheet

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amrsyyssta                                                      70
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<210> 11

<211> 112

<212> PRT

<213> (Unknown) see item 12 on Era Summary Sheet

<400> 11

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L:545 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:545 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:623 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:623 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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